

## Sequence Listing

&lt;110&gt; SUNTORY LIMITED

&lt;120&gt; Glycosyltransferase GnT-V having neovascularization action

&lt;130&gt; DS07F927

&lt;150&gt; PCT/JP02/13879

&lt;151&gt; 2002-12-27

&lt;160&gt; 13

&lt;210&gt; 1

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

Thr Pro Trp Gly Lys

1 5

&lt;210&gt; 2

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Asn Ile Pro Ser Tyr Val

1 5

&lt;210&gt; 3

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn Tyr

1 5 10 15

Ala

&lt;210&gt; 4

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Asp Leu Gln Phe Leu Leu

1

5

&lt;210&gt; 5

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Asn Thr Asp Phe Phe Ile Gly

1

5

&lt;210&gt; 6

&lt;211&gt; 2095

&lt;212&gt; cDNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

CCGGCTGAAG CATCAGAATG GAAGTGAGGA AAGGCAACCA GCTGACACAG  
GAGCCAGAGT 60GAGACCAGCA GACTCTCACA CTCAACCTAC ACCATGAATT TGTGTCTATC  
TTCTACGCGT 120TAAGAGCCAA GGACAGGTGA AGTTGCCAGA GAGCA ATG GCT CTC TTC  
ACT CCG 173

Met Ala Leu Phe Thr Pro

1

5

TGG AAG TTG TCC TCT CAG AAG CTG GGC TTT TTC CTG GTG ACT TTT GGC  
221

Trp Lys Leu Ser Ser Gln Lys Leu Gly Phe Phe Leu Val Thr Phe Gly

10

15

20

TTC ATT TGG GGT ATG ATG CTT CTG CAC TTT ACC ATC CAG CAG CGA ACT  
269

Phe Ile Trp Gly Met Met Leu Leu His Phe Thr Ile Gln Gln Arg Thr  
25 30 35

CAG CCT GAA AGC AGC TCC ATG CTG CGC GAG CAG ATC CTG GAC CTC  
AGC 317

Gln Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser  
40 45 50

AAA AGG TAC ATC AAG GCA CTG GCA GAA GAA AAC AGG AAT GTG GTG  
GAT 365

Lys Arg Tyr Ile Lys Ala Leu Ala Glu Glu Asn Arg Asn Val Val Asp  
55 60 65 70

GGG CCA TAC GCT GGA GTC ATG ACA GCT TAT GAT CTG AAG AAA ACC CTT  
413

Gly Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu  
75 80 85

GCT GTG TTA TTA GAT AAC ATT TTG CAG CGC ATT GGC AAG TTG GAG TCG  
461

Ala Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser  
90 95 100

AAG GTG GAC AAT CTT GTT GTC AAT GGC ACC GGA ACA AAC TCA ACC  
AAC 509

Lys Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn  
105 110 115

TCC ACT ACA GCT GTT CCC AGC TTG GTT GCA CTT GAG AAA ATT AAT GTG  
557

Ser Thr Thr Ala Val Pro Ser Leu Val Ala Leu Glu Lys Ile Asn Val  
120 125 130

GCA GAT ATC ATT AAC GGA GCT CAA GAA AAA TGT GTA TTG CCT CCT ATG  
605

Ala Asp Ile Ile Asn Gly Ala Gln Glu Lys Cys Val Leu Pro Pro Met

135                      140                      145                      150

GAC GGC TAC CCT CAC TGT GAG GGA AAG ATC AAG TGG ATG AAA GAC  
ATG    653

Asp Gly Tyr Pro His Cys Glu Gly Lys Ile Lys Trp Met Lys Asp Met

155                      160                      165

TGG CGT TCA GAT CCC TGC TAC GCA GAC TAT GGA GTG GAT GGA TCC ACC  
701

Trp Arg Ser Asp Pro Cys Tyr Ala Asp Tyr Gly Val Asp Gly Ser Thr

170                      175                      180

TGC TCT TTT TTT ATT TAC CTC AGT GAG GTT GAA AAT TGG TGT CCT CAT  
749

Cys Ser Phe Phe Ile Tyr Leu Ser Glu Val Glu Asn Trp Cys Pro His

185                      190                      195

TTA CCT TGG AGA GCA AAA AAT CCC TAC GAA GAA GCT GAT CAT AAT TCA  
797

Leu Pro Trp Arg Ala Lys Asn Pro Tyr Glu Glu Ala Asp His Asn Ser

200                      205                      210

TTG GCG GAA ATT CGT ACA GAT TTT AAT ATT CTC TAC AGT ATG ATG AAA  
845

Leu Ala Glu Ile Arg Thr Asp Phe Asn Ile Leu Tyr Ser Met Met Lys

215                      220                      225                      230

AAG CAT GAA GAA TTC CGG TGG ATG AGA CTA CGG ATC CGG CGA ATG GCT  
893

Lys His Glu Glu Phe Arg Trp Met Arg Leu Arg Ile Arg Arg Met Ala

235                      240                      245

GAC GCA TGG ATC CAA GCA ATC AAG TCC CTG GCA GAA AAG CAG AAC

CTT 941

Asp Ala Trp Ile Gln Ala Ile Lys Ser Leu Ala Glu Lys Gln Asn Leu

250

255

260

GAA AAG AGA AAG CGG AAG AAA GTC CTC GTT CAC CTG GGA CTC CTG  
ACC 989

Glu Lys Arg Lys Arg Lys Lys Val Leu Val His Leu Gly Leu Leu Thr

265

270

275

AAG GAA TCT GGA TTT AAG ATT GCA GAG ACA GCT TTC AGT GGT GGC CCT  
1037

Lys Glu Ser Gly Phe Lys Ile Ala Glu Thr Ala Phe Ser Gly Gly Pro

280

285

290

CTT GGT GAA TTA GTT CAA TGG AGT GAT TTA ATT ACA TCT CTG TAC TTA  
1085

Leu Gly Glu Leu Val Gln Trp Ser Asp Leu Ile Thr Ser Leu Tyr Leu

295

300

305

310

CTG GGC CAT GAC ATT AGG ATT TCA GCT TCA CTG GCT GAG CTC AAG GAA  
1133

Leu Gly His Asp Ile Arg Ile Ser Ala Ser Leu Ala Glu Leu Lys Glu

315

320

325

ATC ATG AAG AAG GTT GTA GGA AAC CGA TCT GGC TGC CCA ACT GTA GGA  
1181

Ile Met Lys Lys Val Val Gly Asn Arg Ser Gly Cys Pro Thr Val Gly

330

335

340

GAC AGA ATT GTT GAG CTC ATT TAC ATT GAT ATT GTA GGA CTT GCT CAA  
1229

Asp Arg Ile Val Glu Leu Ile Tyr Ile Asp Ile Val Gly Leu Ala Gln

345

350

355

TTC AAG AAA ACT CTT GGA CCA TCC TGG GTT CAT TAC CAG TGC ATG CTC  
1277

Phe Lys Lys Thr Leu Gly Pro Ser Trp Val His Tyr Gln Cys Met Leu  
 360 365 370

CGA GTC CTT GAT TCA TTT GGT ACT GAA CCC GAA TTT AAT CAT GCA AAT  
 1325

Arg Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn  
 375 380 385 390

TAT GCC CAA TCG AAA GGC CAC AAG ACC CCT TGG GGA AAA TGG AAT  
 CTG 1373

Tyr Ala Gln Ser Lys Gly His Lys Thr Pro Trp Gly Lys Trp Asn Leu  
 395 400 405

AAC CCT CAG CAG TTT TAT ACC ATG TTC CCT CAT ACC CCA GAC AAC AGC  
 1421

Asn Pro Gln Gln Phe Tyr Thr Met Phe Pro His Thr Pro Asp Asn Ser  
 410 415 420

TTT CTG GGG TTT GTG GTT GAG CAG CAC CTG AAC TCC AGT GAT ATC CAC  
 1469

Phe Leu Gly Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His  
 425 430 435

CAC ATT AAT GAA ATC AAA AGG CAG AAC CAG TCC CTT GTG TAT GGC AAA  
 1517

His Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys  
 440 445 450

GTG GAT AGC TTC TGG AAG AAT AAG AAG ATC TAC TTG GAC ATT ATT CAC  
 1565

Val Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His  
 455 460 465 470

ACA TAC ATG GAA GTG CAT GCA ACT GTT TAT GGC TCC AGC ACA AAG AAT  
 1613

Thr Tyr Met Glu Val His Ala Thr Val Tyr Gly Ser Ser Thr Lys Asn

475

480

485

ATT CCC AGT TAC GTG AAA AAC CAT GGT ATC CTC AGT GGA CGG GAC CTG  
1661

Ile Pro Ser Tyr Val Lys Asn His Gly Ile Leu Ser Gly Arg Asp Leu

490

495

500

CAG TTC CTT CTT CGA GAA ACC AAG TTG TTT GTT GGA CTT GGG TTC CCT  
1709

Gln Phe Leu Leu Arg Glu Thr Lys Leu Phe Val Gly Leu Gly Phe Pro

505

510

515

TAC GAG GGC CCA GCT CCC CTG GAA GCT ATC GCA AAT GGA TGT GCT TTT  
1757

Tyr Glu Gly Pro Ala Pro Leu Glu Ala Ile Ala Asn Gly Cys Ala Phe

520

525

530

CTG AAT CCC AAG TTC AAC CCA CCC AAA AGC AGC AAA AAC ACA GAC  
TTT 1805

Leu Asn Pro Lys Phe Asn Pro Pro Lys Ser Ser Lys Asn Thr Asp Phe

535

540

545

550

TTC ATT GGC AAG CCA ACT CTG AGA GAG CTG ACA TCC CAG CAT CCT TAC  
1853

Phe Ile Gly Lys Pro Thr Leu Arg Glu Leu Thr Ser Gln His Pro Tyr

555

560

565

GCT GAA GTT TTC ATC GGG CGG CCA CAT GTG TGG ACT GTT GAC CTC AAC  
1901

Ala Glu Val Phe Ile Gly Arg Pro His Val Trp Thr Val Asp Leu Asn

570

575

580

AAT CAG GAG GAA GTA GAG GAT GCA GTG AAA GCA ATT TTA AAT CAG AAG  
1949

Asn Gln Glu Glu Val Glu Asp Ala Val Lys Ala Ile Leu Asn Gln Lys

585

590

595

ATT GAG CCA TAC ATG CCA TAT GAA TTT ACG TGC GAG GGG ATG CTA CAG  
1997

Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys Glu Gly Met Leu Gln  
600 605 610

AGA ATC AAT GCT TTC ATT GAA AAA CAG GAC TTC TGC CAT GGG CAA GTG  
2045

Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe Cys His Gly Gln Val  
615 620 625 630

ATG TGG CCA CCC CTC AGC GCC CTA CAG GTC AAG CTT GCT GAG CCC  
GGG 2093

Met Trp Pro Pro Leu Ser Ala Leu Gln Val Lys Leu Ala Glu Pro Gly  
635 640 645

CC 2095

<210> 7

<211> 16

<212> PRT

<213> Homo sapiens

<400> 7

Lys Ser Leu Ala Glu Lys Gln Asn Leu Glu Lys Arg Lys Arg Lys Lys  
1 5 10 15

<210> 8

<211> 24

<212> cDNA

<213> Artificial Sequence

<220>

<223>

<400> 8

GGGAGTGAGG ATGATGTAGG GAAG 24

<210> 9



<211> 24

<212> cDNA

<213> Artificial Sequence

<220>

<223>

<400> 9

ATGGGGCAGA GGAAGTTACG TTAT

24

<210> 10

<211> 6

<212> PRT

<213> Homo sapiens

<400> 10

Gly Arg Gly Lys Arg Arg

1

5

<210> 11

<211> 6

<212> PRT

<213> Homo sapiens

<223> KRKRKK peptide

<400> 11

Lys Arg Lys Arg Lys Lys

1

5

<210> 12

<211> 6

<212> PRT

<213> Homo sapiens

<223> FSGGPL peptide

<400> 12

Phe Ser Gly Gly Pro Leu

1

5

<210> 13

<211> 5

<212> PRT

<213> Homo sapiens

<400> 13

His Phe Thr Ile Gln

1

5